> **This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.**

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information
 4
 5    (i)  APPLICANT:      Lin et al.
 6
 7    (ii) TITLE OF INVENTION:       Glial Derived Neurotrophic
 8                                   Factor
 9
10    (iii)NUMBER OF SEQUENCES: 24
11
12    (iv) CORRESPONDENCE ADDRESS:
13         (A)   ADDRESSEE: Beaton & Swanson, P.C.
14         (B)   STREET: 4582 South Ulster Street Parkway, Suite
15               #403
16         (C)   CITY:      Denver
17         (D)   STATE:     Colorado
18         (E)   COUNTRY:   USA
19         (F)   ZIP:   80237
20
21    (v)  COMPUTER READABLE FORM:
22         (A)   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
23         (B)   COMPUTER: IBM compatible
24         (C)   OPERATING SYSTEM: MS DOS
25         (D)   SOFTWARE: Wordperfect 5.1
26
27    (vi) CURRENT APPLICATION DATA:
28         (A)   APPLICATION NUMBER:  08/182,183
29         (B)   FILING DATE:  5-MAY-1994
30
31    (vii) PRIOR APPLICATION DATA:
32         (A)   APPLICATION NUMBER: 07/788,423, 07/774,109,
33               07/764,685
34         (B)   FILING DATE:   06-NOV-1991, 08-OCT-1991, 20-SEP-
35                              1991
36
37    (viii) ATTORNEY/AGENT INFORMATION:
38         (A)   NAME: Barry J. Swanson
39         (B)   REGISTRATION NUMBER: 33,215
40         (C)   REFERENCE/DOCKET NUMBER:  SYNE-225C
41
42    (ix) TELECOMMUNICATION INFORMATION:
43         (A)   TELEPHONE: (303) 850-9900
44         (B)   TELEFAX: (303) 850-9401
45
```

INPUT SET: S354.raw

ERRORED SEQUENCES FOLLOW:

```
78    (2)  INFORMATION FOR SEQ ID NO:3
79
80         (i)  SEQUENCE CHARACTERISTICS:
81              (A)  LENGTH: 900 base pairs
82              (B)  TYPE: nucleic acid
83              (C)  STRANDEDNESS: single
84              (D)  TOPOLOGY: linear
85
86         (ix) FEATURE:
87              (A)  NAME/KEY: nucleic acid for rat GDNF
88
89         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
90
91    CCCCCGGGCT GCAGGAATTC GGGG GTC TAC GGA GAC CGG ATC CGA GGT GCC
92    GCC                                                                          54
93                         Val Tyr Gly Asp Arg Ile Arg Gly Ala
94    Ala
95                                       -90                    -85
96
97    GCC GGA CGG GAC TCT AAC ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC    102
98    Ala Gly Arg Asp Ser Lys Met Lys Leu Trp Asp Val Val Ala Val Cys
99                 -80              -75              -70
100
101   CTG GTG TTG CTG CAC ACC GCG TCT GCC TTC CCG CTG CCC GCC GGT AAG    150
102   Leu Val Leu Leu His Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys
103              -65              -60              -55
104
105   AGG CTT CTC GAA GCG CCC GCC GAA GAC CAC TCC CTC GGC CAC CGC CGC    198
106   Arg Leu Leu Glu Ala Pro Ala Glu Asp His Ser Leu Gly His Arg Arg
107       -50              -45              -40
108
109   GTG CCC TTC GCG CTG ACC AGT GAC TCC AAT ATG CCC GAA GAT TAT CCT    246
110   Val Pro Phe Ala Leu Thr Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro
111   -35              -30              -25              -20
112
113   GAC CAG TTT GAT GAC GTC ATG GAT TTT ATT CAA GCC ACC ATC AAA AGA    296 294
114   Asp Gln Phe Asp Asp Val Met Asp Phe Ile Gln Ala Thr Ile Lys Arg
115              -15              -10              -5
116
117   CTG AAA AGG TCA CCA GAT AAA CAA GCG GCG GCA CTT CCT CGA AGA GAG    342
118   Leu Lys Arg Ser Pro Asp Lys Gln Ala Ala Ala Leu Pro Arg Arg Glu
119              1                5                10
120
121   AGG AAC CGG CAA GCT GCA GCT GCC AGC CCA GAG AAT TCC AGA GGG AAA    390
122   Arg Asn Arg Gln Ala Ala Ala Ala Ser Pro Glu Asn Ser Arg Gly Lys
123       15               20               25
124
```

INPUT SET: S354.raw

```
125   GGT CGC AGA GGC CAG AGG GGC AAA AAT CGG GGG TGC GTC TTA ACT GCA          438
126   Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala
127    30                  35                  40                  45

128
129   ATA CAC TTA AAT GTC ACT GAC TTG GGT TTG GGC TAC GAA ACC AAG GAG          486
130   Ile His Leu Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu
131                    50                  55                  60

132
133   GAA CTG ATC TTT CGA TAT TGT AGC GGT TCC TGT GAA GCG GCC GAG ACA          534
134   Glu Leu Ile Phe Arg Tyr Cys Ser Gly Ser Cys Glu Ala Ala Glu Thr
135                    65                  70                  75

136
137   ATG TAC GAC AAA ATACTA AAA AAT CTG TCT CGA AGT AGA AGG CTA ACA           582
138   Met Tyr Asp Lys Ile Leu Lys Asn Leu Ser Arg Ser Arg Arg Leu Thr
139                    80                  85                  90

140
141   AGT GAC AAG GTA GGC CAG GCA TGT TGC AGG CCG GTC GCC TTC GAC GAC          630
142   Ser Asp Lys Val Gly Gln Ala Cys Cys Arg Pro Val Ala Phe Asp Asp
143        95                  100                 105

144
145   GAC CTG TCG TTT TTA GAC GAC AGC CTG GTT TAC CAT ATC CTA AGA AAG          678
146   Asp Leu Ser Phe Leu Asp Asp Ser Leu Val Tyr His Ile Leu Arg Lys
147   110                 115                 120                 125

148
149   CAT TCC GCT AAA CGG TGT GGA TGT ATC TGA CCCTGGCTCC AGAGACTGCT           728
150   His Ser Ala Lys Arg Cys Gly Cys Ile
151                    130

152
153   GTGTATTGCA TTCCTGCTAC ACTGCGAAGA AAGGGACCAA GGTTCCCAGG
154   AAATATTTGC                                                              788

155
156   CCAGAAAGGA AGATAAGGAC CAAGAAGGCA GAGGCAGAGG CGGAAGAAGA
157   AGAAGAAAAG                                                              848

158
159   AAGGACGAAG GCAGCCATCT GTGGGAGCCT GTAGAAGGAG GCCCAGCTAC AG              900
160
161
```

insert a nucleic on each line

```
316   (2)  INFORMATION FOR SEQ ID NO:8
317
318        (i)   SEQUENCE CHARACTERISTICS:
319              (A)   LENGTH: 223 base pairs
320              (B)   TYPE: nucleic acid
321              (C)   STRANDEDNESS: single
322              (D)   TOPOLOGY: linear
323
324        (ix) FEATURE:
325              (A)   NAME/KEY: nucleic acid sequence for human GDNF
326
327        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
328
329   TTCTCTCCCC CACCTCCCGC CTGCCCGCGC A GGT GCC GCC GCC GGA CGG GAC
330   TTT                                                                     55
```

INPUT SET: S354.raw

```
331                                              Gly Ala Ala Ala Gly Arg Asp
332    Phe
333                                                             -5
334
335    AAG ATG AAG TTA TGG GAT GTC GTG GCT GTC TGC CTG GTG CTG CTC CAC          103
336    Lys Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His
337         1               5                   10                  15
338
339    ACC GCG TCC GCC TTC CCG CTG CCC GCC GGT AAG AGG CCT CCC GAG GCG          151
340    Thr Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala
341                        20                  25                  30
342
343    CCC GCC GAA GAC CGC TCC CTC GGC CGC CGC CGC GCG CCC TTC GCG CTG          199
344    Pro Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu
345                        35                  40                  45
346
347    AGC AGT GAC TGTAAGAACC GTTCC                                            223
348    Ser Ser Asp
349                50
350
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/182,183A*

INPUT SET: S354.raw

Line	Error	Original Text
81	Entered (900) and Calc. Seq. Length (749) differ	(A) LENGTH: 900 base pairs
92	# of Sequences for line conflicts w/ running total	GCC
113	# of Sequences for line conflicts w/ running total	GAC CAG TTT GAT GAC GTC ATG GAT TTT ATT CA
117	# of Sequences for line conflicts w/ running total	CTG AAA AGG TCA CCA GAT AAA CAA GCG GCG G
154	# of Sequences for line conflicts w/ running total	AAATATTTGC
157	# of Sequences for line conflicts w/ running total	AGAAGAAAAG
319	Entered (223) and Calc. Seq. Length (171) differ	(A) LENGTH: 223 base pairs
330	# of Sequences for line conflicts w/ running total	TTT